

GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: March 11, 2003, 23:09:45 ; Search time 53 Seconds  
(without alignments)  
2516.677 Million cell updates/sec

Title: US-10-046-433-40  
Perfect score: 5506  
Sequence: 1 MAEPGSHHLSARVQRTTER.....LGRSHNLPPRGLMLDTCCR 1001

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: A.Geneseq\_101002:\*  
2: /SID2/gcgdata/geneseq/genesep-emb1/AA1980.DAT.\*  
3: /SID2/gcgdata/geneseq/genesep-emb1/AA1981.DAT.\*  
4: /SID2/gcgdata/geneseq/genesep-emb1/AA1982.DAT.\*  
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23: /SID2/gcgdata/geneseq/genesep-emb1/AA2001.DAT.\*  
24: /SID2/gcgdata/geneseq/genesep-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5506	100.0	1001	22	Human TR13 recepto
2	5376	97.6	1013	22	Human CASB619 prot
3	5363	97.4	1013	22	Human acid sequenc
4	5341	97.0	1013	22	Human PRO4985 poly
5	5005	90.9	911	22	Amino acid sequenc
6	4784	86.9	870	22	Amino acid sequenc
7	3870	70.3	750	22	Human TR13 recepto
8	2982.5	54.2	1027	22	Human TR16-10ng recepto
9	2815.5	51.1	963	22	Human TR16-short recepto
10	2491	45.2	495	20	Human endometrium

11	2119	38.5	383	22	AAB83853	Amino acid sequenc
12	1761.5	32.0	372	22	AAB85768	Human seven-transm
13	1448	26.3	464	22	AAB48377	Human SEC10 protei
14	1307.5	23.7	411	22	AAB48372	Human SEC5 protein
15	1169	21.2	209	22	AAB83852	Amino acid sequenc
16	889.5	16.2	208	21	AAB53442	Human colon cancer
17	776	14.1	147	22	AAB83849	Peptide fragment o
18	710	12.9	150	20	AA112274	Human 5' EST secre
19	518	9.4	105	21	AAB26180	Human CASB619 prot
20	325	5.9	36	22	AAB83847	Peptide fragment o
21	284	5.2	74	22	AAB70281	Peptide #25. Unid
22	273	5.0	81	22	ABB39918	Peptide #7424 enco
23	273	5.0	81	22	ABB24471	Protein #6470 enco
24	273	5.0	81	22	AAW60663	Human bone marrow
25	273	5.0	81	22	AAW73335	Human brain expres
26	273	5.0	81	22	AAW33535	Human bone marrow
27	273	5.0	81	22	ABG43166	Peptide #7572 enco
28	269	4.9	52	23	ABG3848	Human peptide enco
29	252	4.6	1576	21	AAAB19802	Peptide fragment o
30	252	4.6	1576	21	AAAB48453	Human laminin 2 ma
31	252	4.6	1576	23	ABB81595	Human laminin 10 t
32	252	4.6	1584	21	AAAB19804	Human laminin 2 ga
33	252	4.6	1609	21	AAAB48452	Human laminin 2 ga
34	252	4.6	1609	21	AAAB19801	Human laminin 2 ga
35	252	4.6	1609	23	ABB81594	Human laminin 2 ga
36	252	4.6	1617	21	AAAB19803	Human laminin 2 ga
37	251	4.6	1609	19	AAW50898	Human laminin 2 ga
38	244	4.4	45	22	AAAB3846	Human laminin GI C
39	233	4.2	3594	23	AAE20147	Peptide fragment o
40	229.5	4.2	1572	21	AAAB19805	Mouse C3b/C4b comp
41	229.5	4.2	1572	21	AAAB48455	Mouse laminin 2 ma
42	229.5	4.2	1572	23	ABB81597	Mouse laminin 8 po
43	229.5	4.2	1605	21	AAAB19805	Mouse laminin 10 t
44	229.5	4.2	1605	21	AAAB48454	Mouse laminin 2 ga
45	229.5	4.2	1605	23	ABB81596	Mouse laminin 10 t

## ALIGNMENTS

RESULT 1  
ID AAB35333 standard; Protein: 1001 AA.  
AC AAB35333;  
XX 08-MAY-2001 (first entry)  
XX  
XX Human TR13 receptor protein SEQ ID NO: 40.  
XX  
XX Human; tumour necrosis factor receptor; TR13; TR14; infection;  
XX cancer; autoimmune disease; allergy; inflammatory disease;  
XX graft rejection; apoptosis; cardiovascular disease; aneurysm.  
XX  
XX OS Homo sapiens.  
XX  
XX WO200105834-A1.  
XX  
XX 25-JAN-2001.  
XX  
XX 14-JUL-2000; 2000WO-US19343.  
XX  
XX 16-JUL-1999; 99US-0144087.  
XX 18-AUG-1999; 99US-0149450.  
XX 20-AUG-1999; 99US-0149712.  
XX 10-SEP-1999; 99US-0153089.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Ruben SM, Ni J, Young PE;  
XX WPI; 2001-112682/12.  
XX

PT Nucleic acids encoding 2 human tumor necrosis factor receptor  
 PT polypeptides (TR13) and (TR14)), useful for the prevention, diagnosis  
 PT and treatment of, e.g., cancers, acquired immune deficiency syndrome and  
 PT hypohidrotic ectodermal dysplasia -

XX Claim 40; Page 398-401; 418pp; English.

CC The present invention provides the protein and coding sequences of the  
 CC human tumor necrosis factor receptors TR13 and TR14. These sequences are  
 CC useful in the diagnosis and treatment of many diseases, including cancer,  
 CC autoimmune diseases, cardiovascular disorders, allergies,  
 CC neurodegenerative diseases, graft rejection, inflammation, aneurysms and  
 CC infections.

XX Sequence 1001 AA;

Query Match 100.0%; Score 5506; DB 22; Length 1001;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEPGSHHLSARVGRTERIRIPRLMRLLMAGTAFOVTOGTGPELHACKSEHYEYTA 60  
 DB 1 MAEPGSHHLSARVGRTERIRIPRLMRLLMAGTAFOVTOGTGPELHACKSEHYEYTA 60  
 QY 61 CDSTGSRMRVAVPHPTGCLTSLPDPVKGTEGSCFNAGEFLDMKDQSCPCAEGRYSIGT 120  
 DB 61 CDSTGSRMRVAVPHPTGCLTSLPDPVKGTEGSCFNAGEFLDMKDQSCPCAEGRYSIGT 120  
 QY 121 G1RFDEMDLPHGFASLSANMELDDSAESTNCSTSKWVRGDIYANTDECTATLMTYA 180  
 DB 121 G1RFDEMDLPHGFASLSANMELDDSAESTNCSTSKWVRGDIYANTDECTATLMTYA 180  
 QY 181 VMLKOSGTNFEYYPDSIIIEFFVQNDQCPNADDSRMWKTTEKGEHFSEVLNNGNN 240  
 DB 181 VMLKOSGTNFEYYPDSIIIEFFVQNDQCPNADDSRMWKTTEKGEHFSEVLNNGNN 240  
 QY 241 VLYMRTAFSVTKPKPVLVRLNLTATGVAATSECFPEKPTYADKQSSFCILCPANSTY 300  
 DB 241 VLYMRTAFSVTKPKPVLVRLNLTATGVAATSECFPEKPTYADKQSSFCILCPANSTY 300  
 QY 301 SNGKGETSCHODCPDKYSKSGSSCNVRPACTDKDYFYTHACDANGETOLMTYMAKPKTC 360  
 DB 301 SNGKGETSCHODCPDKYSKSGSSCNVRPACTDKDYFYTHACDANGETOLMTYMAKPKTC 360  
 QY 361 SEDLEGAYKLPAASGVKTHPCPNCGFEKTNNTQPCPYGYSYNGSDCTRCPAETPAVG 420  
 DB 361 SEDLEGAYKLPAASGVKTHPCPNCGFEKTNNTQPCPYGYSYNGSDCTRCPAETPAVG 420  
 QY 421 FEYKMWNTLPTNMTETVLSGINFYKMGTMGVAAGDHIYTAAGASNDPMILTLVPGFR 480  
 DB 421 FEYKMWNTLPTNMTETVLSGINFYKMGTMGVAAGDHIYTAAGASNDPMILTLVPGFR 480  
 QY 481 PROSVMADEKKEVARTTFEFLICSYNCLYMGVNSRNTPEVTMGSKGKGSYTYI 540  
 DB 481 PROSVMADEKKEVARTTFEFLICSYNCLYMGVNSRNTPEVTMGSKGKGSYTYI 540  
 QY 541 IEEHTTTSFTWAFORTTFHASKRYNDVAKIYSINVTVMNGVASYCPALAEASDVGS 600  
 DB 541 IEEHTTTSFTWAFORTTFHASKRYNDVAKIYSINVTVMNGVASYCPALAEASDVGS 600  
 QY 601 SCGSCPAGIYIDRDSGTHSCPNITLKAHOPGVQACVPCGPGTKNNKIHSLCYNDCIF 660  
 DB 601 SCGSCPAGIYIDRDSGTHSCPNITLKAHOPGVQACVPCGPGTKNNKIHSLCYNDCIF 660  
 QY 661 SRNPTPTFENYNSALANTVTLAAGSPSTSKLAKYFHHHTLSLGNQGRKMSVCTDNTD 720  
 DB 661 SRNPTPTFENYNSALANTVTLAAGSPSTSKLAKYFHHHTLSLGNQGRKMSVCTDNTD 720  
 QY 721 LRIPBEGSGFSKSTAYVQCAVILPEVYGYKAGVSSQPSVLADLLIYVTDMLTLDGTS 780  
 DB 721 LRIPBEGSGFSKSTAYVQCAVILPEVYGYKAGVSSQPSVLADLLIYVTDMLTLDGTS 780  
 QY 781 PALFLHLSLGIPIVDYIEFRSDNYQSCSGRSTTIRVRCSPQTVPGSILLPGTCSDGT 840

DB 781 PALFLHLSLGIPIVDYIEFRSDNYQSCSGRSTTIRVRCSPQTVPGSILLPGTCSDGT 840  
 QY 841 CDGCFHFHLESAAACPLCSVADYHAIVSSCVAGICKTYYVREPKLCSGSLPEQRYT 900  
 DB 841 CDGCFHFHLESAAACPLCSVADYHAIVSSCVAGICKTYYVREPKLCSGSLPEQRYT 900  
 QY 901 ICKTIDFWLKVGISAGCTAIIITLVTCYFWMKNOKLEKYSKLVNMTLKKCDLPAADS 960  
 DB 901 ICKTIDFWLKVGISAGCTAIIITLVTCYFWMKNOKLEKYSKLVNMTLKKCDLPAADS 960  
 QY 961 CAIMEGEDVEDDLIFTSKNHSLGRSNHLPRLGLMDLTQCR 1001  
 DB 961 CAIMEGEDVEDDLIFTSKNHSLGRSNHLPRLGLMDLTQCR 1001

RESULT 2  
 AAB26179  
 ID AAB26179 standard; Protein; 1013 AA.

AC AAB26179;  
 DT 12-FEB-2001 (first entry)  
 DE Human CASB619 protein #1.  
 KW Human; CASB619; cancer; autoimmune disease; immunogen; vaccine;  
 OS Homo sapiens.  
 PN WO200058460-A2.  
 PD 05-OCT-2000.  
 PF 20-MAR-2000; 2000WO-EP02478.  
 PR 26-MAR-1999; 99GB-00077113.  
 PR 25-SEP-1999; 99GB-0022858.  
 PA (SMIR ) SMITHKLINE BEECHAM BIOLOGICALS.

PI Bruck CEM, Cassart J, Coche T, Vinals De Bassols YC;  
 DR WPI: 2000-664923/64.  
 DR N-PSDB: AAA95442.  
 XX Novel CASB619 polypeptides useful for diagnosing, and as vaccines for  
 PT prophylactic and therapeutic treatment of, cancers, particularly  
 PT ovarian and colon carcinoma, and autoimmune diseases -

XX Claim 4; Page 54-56; 68pp; English.  
 CC The present sequence comprises the human CASB619 protein sequence. This  
 CC protein is thought to be specifically or over-expressed in tumor cells,  
 CC and so can be used as a target for antigen-specific immune responses  
 CC which can cause destruction of the tumor cell. In addition, the protein  
 CC and gene can be used in cancer diagnosis, in the treatment of autoimmune  
 CC diseases and in vaccines against cancer and autoimmune disease. The  
 CC invention provides a number of epitopes derived from the protein which  
 CC can be used as immunogens.

XX Sequence 1013 AA;

Query Match 97.6%; Score 5376; DB 21; Length 1013;  
 Best Local Similarity 99.4%; Pred. No. 0;  
 Matches 978; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAEPGSHHLSARVGRTERIRIPRLMRLLMAGTAFOVTOGTGPELHACKSEHYEYTA 60  
 DB 1 MAEPGSHHLSARVGRTERIRIPRLMRLLMAGTAFOVTOGTGPELHACKSEHYEYTA 60  
 QY 61 CDSTGSRMRVAVPHPTGCLTSLPDPVKGTEGSCFNAGEFLDMKDQSCPCAEGRYSIGT 120

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Db      61  CDSTGRMWRVAVPHRTGCLTSLPDPYKGTCECSFSCNAGEFLDMKQOSKPCAEGRYSLGT 120
      121  GTRFDEMDLPHGFASLSANMELDSDAESTGCTSSKWPVRGDIYAFNTDECTATLMA 180
      121  GTRFDEMDLPHGFASLSANMELDSDAESTGCTSSKWPVRGDIYAFNTDECTATLMA 180
      181  VNLKSGIVNFEYYPDSSIIIEFFVQNDQCPNADDSRMKTKTEKGWGFHSVELNRGN 240
      181  VNLKSGIVNFEYYPDSSIIIEFFVQNDQCPNADDSRMKTKTEKGWGFHSVELNRGN 240
      181  VNLKSGIVNFEYYPDSSIIIEFFVQNDQCPNADDSRMKTKTEKGWGFHSVELNRGN 240
      241  VLYWRTTASVWTKPKPVLYVNIATITGAATSECPCKPGIYADKQSSFCILCPANSY 300
      241  VLYWRTTASVWTKPKPVLYVNIATITGAATSECPCKPGIYADKQSSFCILCPANSY 300
      241  VLYWRTTASVWTKPKPVLYVNIATITGAATSECPCKPGIYADKQSSFCILCPANSY 300
      301  SNKGESCHQCPDCKSEKSSSCNVRPACTDKDYFYTTACDANGETOIMTKAPKIC 360
      301  SNKGESCHQCPDCKSEKSSSCNVRPACTDKDYFYTTACDANGETOIMTKAPKIC 360
      301  SNKGESCHQCPDCKSEKSSSCNVRPACTDKDYFYTTACDANGETOIMTKAPKIC 360
      361  SEDLEGAVKLPAAGVYTHCPNPGFFKTNNSTCOPCPYGYTSNGSDCTRCAGTEPAVG 420
      361  SEDLEGAVKLPAAGVYTHCPNPGFFKTNNSTCOPCPYGYTSNGSDCTRCAGTEPAVG 420
      361  SEDLEGAVKLPAAGVYTHCPNPGFFKTNNSTCOPCPYGYTSNGSDCTRCAGTEPAVG 420
      421  FEKKMNNTLPTNMTETVLSGINSKMGWAGDHITTAAGASNDPMILTLVYVGR 480
      421  FEKKMNNTLPTNMTETVLSGINSKMGWAGDHITTAAGASNDPMILTLVYVGR 480
      421  FEKKMNNTLPTNMTETVLSGINSKMGWAGDHITTAAGASNDPMILTLVYVGR 480
      481  POSVADTENKEVARITFEVETLCSVNCLEYFMVGVNSRTNTPVETWKSKGKOSYTYI 540
      481  POSVADTENKEVARITFEVETLCSVNCLEYFMVGVNSRTNTPVETWKSKGKOSYTYI 540
      481  POSVADTENKEVARITFEVETLCSVNCLEYFMVGVNSRTNTPVETWKSKGKOSYTYI 540
      541  IEENTTTSTFWAQRTTFHEASRKYNDVAKIYSTVNTVMNGVASYCPCLASDVGS 600
      541  IEENTTTSTFWAQRTTFHEASRKYNDVAKIYSTVNTVMNGVASYCPCLASDVGS 600
      541  IEENTTTSTFWAQRTTFHEASRKYNDVAKIYSTVNTVMNGVASYCPCLASDVGS 600
      601  SCSCPAAGYIYDRDSCGTHSCSPNTILKAHOPYGVQACVPCGPTKNNKTHSLCYNDCTF 660
      601  SCSCPAAGYIYDRDSCGTHSCSPNTILKAHOPYGVQACVPCGPTKNNKTHSLCYNDCTF 660
      601  SCSCPAAGYIYDRDSCGTHSCSPNTILKAHOPYGVQACVPCGPTKNNKTHSLCYNDCTF 660
      661  SRNPTRTFNYNSALANTVTLAGSPSTSKGLYHHTLSLSCGNGKRMVCTDNDVD 720
      661  SRNPTRTFNYNSALANTVTLAGSPSTSKGLYHHTLSLSCGNGKRMVCTDNDVD 720
      661  SRNPTRTFNYNSALANTVTLAGSPSTSKGLYHHTLSLSCGNGKRMVCTDNDVD 720
      721  LRPEGSGFSKSTIYVCOAVIIPPEVGYKAGVSOPSLADRLIGVTTDLTGITS 780
      721  LRPEGSGFSKSTIYVCOAVIIPPEVGYKAGVSOPSLADRLIGVTTDLTGITS 780
      721  LRPEGSGFSKSTIYVCOAVIIPPEVGYKAGVSOPSLADRLIGVTTDLTGITS 780
      781  PAELFHLESIGIPDYIFFYRSNDVTOSSSGRSTTIRVRCSPQKTVPGSLLPCTSDGT 840
      781  PAELFHLESIGIPDYIFFYRSNDVTOSSSGRSTTIRVRCSPQKTVPGSLLPCTSDGT 840
      781  PAELFHLESIGIPDYIFFYRSNDVTOSSSGRSTTIRVRCSPQKTVPGSLLPCTSDGT 840
      841  CDGCFHFLWESAACPLCSVADYHAIVSSVAGIOKTTYVMREPLKCSGISLPPORAT 900
      841  CDGCFHFLWESAACPLCSVADYHAIVSSVAGIOKTTYVMREPLKCSGISLPPORAT 900
      841  CDGCFHFLWESAACPLCSVADYHAIVSSVAGIOKTTYVMREPLKCSGISLPPORAT 900
      901  ICKTIDFWLVGJSAGCTAIIITLVLCYFMKKNOKLEYKSKLYVMNATLKDCLDPAADS 960
      901  ICKTIDFWLVGJSAGCTAIIITLVLCYFMKKNOKLEYKSKLYVMNATLKDCLDPAADS 960
      901  ICKTIDFWLVGJSAGCTAIIITLVLCYFMKKNOKLEYKSKLYVMNATLKDCLDPAADS 960
      961  CAIMEGEDVEDDLIFTSKNSLGR 984
      961  CAIMEGEDVEDDLIFTSKNSLGR 984
      961  CAIMEGEDVEDDLIFTSKNSLGR 984

```

RESULT 3  
 AAB83845  
 ID AAB83845 standard; Protein; 1013 AA.  
 AC AAB83845;  
 XX  
 DT 23-JUL-2001 (first entry)  
 XX Amino acid sequence of a human protein expressed in tumour cells.

```

XX      "Tumour cell; immunological disease; autoimmune disease; cancer;
KW      Infection.
KW      Homo sapiens.
OS      Homo sapiens.
XX      Key
FH      Peptide
FT      1..41
FT      /note= "signal peptide"
FT      Domain
FT      42..911
FT      /note= "extracellular domain"
FT      Domain
FT      912..930
FT      /note= "transmembrane domain"
FT      Domain
FT      931..1013
FT      /note= "transmembrane domain"
XX      WO200131003-A1.
XX      03-MAY-2001.
XX      30-OCT-2000; 2000WO-FR03032.
XX      29-OCT-1999; 99FR-0013629.
XX      (FABR ) FABRE MEDICAMENT SA PIERRE.
XX      DeIneste Y, Magistrelli G, Jeannin P, Bonnefoy J;
XX      WP1: 2001-328651/34.
XX      N-PSDB; AAF89765.
XX      New nucleic acid, expressed in tumours and lymphoid tissue is useful for
XX      identifying agents for treating tumours and autoimmune disease
XX      Claim 9; Page 48-51; 85pp; French.
XX      The present sequence represents a human protein expressed in tumour
XX      cells. The polynucleotide is useful for screening cDNA/genomic DNA banks
XX      and for cloning isolated DNA; identifying mutant forms of the gene that
XX      encodes a human protein, where the mutations are associated with
XX      abnormal gene expression, or promoters and regulators of the gene,
XX      particularly for diagnosis; for recombinant expression of the derived
XX      protein; as probes and primers for detection and amplification; and
XX      as antisense therapeutics. The tumour expressed protein is useful for
XX      raising specific antibodies and to screen agents that modulate its
XX      activity, bind to it or interact with it. These agents are potentially
XX      useful for treatment or prevention of diseases associated with abnormal
XX      expression/activity of the protein, particularly immunological diseases
XX      (autoimmune diseases and cancer) or viral, bacterial, fungal or parasitic
XX      infections.
XX      Sequence 1013 AA;
XX      Query Match 97.4%; Score 5363; DB 22; Length 1013;
XX      Best Local Similarity 99.2%; Pred. No. 0;
XX      Matches 976; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
XX      1 MAEPGSHLSARVGRTERRTIRLRLMLMAGTAFOYTGTPGLHACKSESEHYEYTA 60
XX      1 MAEPGSHLSARVGRTERRTIRLRLMLMAGTAFOYTGTPGLHACKSESEHYEYTA 60
XX      61 CDSTGRMWRVAVPHRTGCLTSLPDPYKGTCECSFSCNAGEFLDMKQOSKPCAEGRYSLGT 120
XX      61 CDSTGRMWRVAVPHRTGCLTSLPDPYKGTCECSFSCNAGEFLDMKQOSKPCAEGRYSLGT 120
XX      121 GTRFDEMDLPHGFASLSANMELDSDAESTGCTSSKWPVRGDIYAFNTDECTATLMA 180
XX      121 GTRFDEMDLPHGFASLSANMELDSDAESTGCTSSKWPVRGDIYAFNTDECTATLMA 180
XX      181 VNLKSGIVNFEYYPDSSIIIEFFVQNDQCPNADDSRMKTKTEKGWGFHSVELNRGN 240
XX      181 VNLKSGIVNFEYYPDSSIIIEFFVQNDQCPNADDSRMKTKTEKGWGFHSVELNRGN 240
XX      181 VNLKSGIVNFEYYPDSSIIIEFFVQNDQCPNADDSRMKTKTEKGWGFHSVELNRGN 240

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[illegible]

XX 01-DEC-2000; 2000WO-US32678.  
PE  
XX  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 09-DEC-1999; 99US-0170262.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 20-DEC-1999; 99WO-US30999.  
PR 30-DEC-1999; 99WO-US31243.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 11-FEB-2000; 2000WO-US00376.  
PR 18-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04342.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 10-NOV-2000; 2000WO-US30873.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AU, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX  
XX WPI: 2001-408281/43.  
DR N-PSDB; AAS21262.  
XX  
PT Isolated, secretory and transmembrane PRO polypeptide used to detect  
PT other PRO polypeptides, link bioactive molecules to cells expressing  
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
PT lung, breast, prostate, cervical  
XX  
XX Claim 12; Fig 38; 813pp; English.  
XX  
XX AAU012172-AAU12446 represent novel human secretory and transmembrane  
CC PRO polypeptides. The PRO polypeptides are useful to detect other  
CC PRO polypeptides, to link bioactive molecules to cells expressing  
CC PRO polypeptides, to modulate biological activities of cells expressing  
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
CC polypeptide expression in a cell sample to that in a control sample.  
CC Some of the 275 sequences are also useful to stimulate the release of  
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
CC proliferation or differentiation of chondrocytes, the proliferation or  
CC gene expression in pericyte cells, the release of proteoglycans from  
CC cartilage, the proliferation of inner ear utricular supporting cells or  
CC of T-lymphocytes, the release of a cytokine from peripheral blood  
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by  
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
CC to factor VITA. The PRO polypeptides can be used in assays to identify  
CC molecules involved in binding interactions. The polynucleotides encoding  
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
CC transgenic or knock out animals and can be used in gene therapy.  
XX  
XX Sequence 1013 AA;  
SQ  
Query Match 97.0%; Score 5341; DB 22; Length 1013;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 974; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

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OY 1 MAEPGHSHLSARVGRTERRIRPLMLLLMAGTAQVOTGTGPELHACKESYHEYYTA 60
DB 1 MAEPGHSHLSARVGRTERRIRPLMLLLMAGTAQVOTGTGPELHACKESYHEYYTA 60
OY 61 CDSTGSRMRVAVPHPTPGICTSLPDPVKGTECSFSCNAGEFLDMKDCSCPCAGRSYSLGT 120
DB 61 CDSTGSRMRVAVPHPTPGICTSLPDPVKGTECSFSCNAGEFLDMKDCSCPCAGRSYSLGT 120
OY 121 GIREDEMDLPHGFASLSANMELDLSAAESTGNTSSKWPVRGDIYAFNDECTATLMTA 180
DB 121 GIREDEMDLPHGFASLSANMELDLSAAESTGNTSSKWPVRGDIYAFNDECTATLMTA 180
OY 181 VNLKOSGTVNFEXYYPDSIIIFEEFVONDQCPNADSRMMKTTTEKMEFHSVELNRGN 240
DB 181 VNLKOSGTVNFEXYYPDSIIIFEEFVONDQCPNADSRMMKTTTEKMEFHSVELNRGN 240
OY 241 VLYWRTAFSVTKVPKPLVRLNIAITGVAYTSECFPCPKGTADKOGSSFCCLCPANSY 300
DB 241 VLYWRTAFSVTKVPKPLVRLNIAITGVAYTSECFPCPKGTADKOGSSFCCLCPANSY 300
OY 301 SNKGTSCHQCDPDKYSEKSSCNVPRACDCKDFTYHTACDANGETQLMKAKRKIC 360
DB 301 SNKGTSCHQCDPDKYSEKSSCNVPRACDCKDFTYHTACDANGETQLMKAKRKIC 360
OY 361 SEDLEGAVALPASGVKTHCPNPGFETKNNSTCPCPYGYSNGSDCTRCPCATEPAVG 420
DB 361 SEDLEGAVALPASGVKTHCPNPGFETKNNSTCPCPYGYSNGSDCTRCPCATEPAVG 420
OY 421 FEYKMNNTLPTNMTTSLGNEFYKMTGMEVADHITYAAGASDNDPMLTLTVPEGR 480
DB 421 FEYKMNNTLPTNMTTSLGNEFYKMTGMEVADHITYAAGASDNDPMLTLTVPEGR 480
OY 481 PPSVMAADENKVARITVEFETLSCNCELFMYGVNSRNTPEYTKGSKGOSYTYI 540
DB 481 PPSVMAADENKVARITVEFETLSCNCELFMYGVNSRNTPEYTKGSKGOSYTYI 540
OY 541 IEBNTTTSPTWAFQRTTFHESAKRYNDVAKIYSINVTVMNGVASYSYCPCLASDVGS 600
DB 541 IEBNTTTSPTWAFQRTTFHESAKRYNDVAKIYSINVTVMNGVASYSYCPCLASDVGS 600
OY 601 SCTSCPRAGYIIRDSGCHSCPNNTLLKAHOPYGVACPCPGCTKNNKIHSLCYNDCTF 660
DB 601 SCTSCPRAGYIIRDSGCHSCPNNTLLKAHOPYGVACPCPGCTKNNKIHSLCYNDCTF 660
OY 661 SRNPTRTFNFNFSALANTVTLAGGPFSTSKGLTFHFTLSLSCGNGRKSVCYTDNVT 720
DB 661 SRNPTRTFNFNFSALANTVTLAGGPFSTSKGLTFHFTLSLSCGNGRKSVCYTDNVT 720
OY 721 LRIPEGESGFSKITAYVCAVLIIPREVTGYKAGVSSOPVSLADRLIGVTTDMLDGLTS 780
DB 721 LRIPEGESGFSKITAYVCAVLIIPREVTGYKAGVSSOPVSLADRLIGVTTDMLDGLTS 780
OY 781 PAELFHESLGIPVIFEFYRNDVTOSSGSRSTTIVRCSPOKTVPGSLLLEGTSDDCT 840
DB 781 PAELFHESLGIPVIFEFYRNDVTOSSGSRSTTIVRCSPOKTVPGSLLLEGTSDDCT 840
OY 841 CDGCFHFLMESAAACPLCSVADYHAIVSSCVAGIQKTTYVMBEPKLCSSGISLPPORAT 900
DB 841 CDGCFHFLMESAAACPLCSVADYHAIVSSCVAGIQKTTYVMBEPKLCSSGISLPPORAT 900
OY 901 ICKTIDFMLKYGISAGTCTALLVLCYFPMKKNOKLEFYKSKLYMNAATLKDCLPAADS 960
DB 901 ICKTIDFMLKYGISAGTCTALLVLCYFPMKKNOKLEFYKSKLYMNAATLKDCLPAADS 960
OY 961 CAIMEGEDEVEDLIFTSKNHSIGR 984
DB 961 CAIMEGEDEVEDLIFTSKNHSIGR 984

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RESULT 5  
AAB83850  
AAB83850 standard; Protein; 911 AA.

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XX AAB83850;
AC 23-JUL-2001 (first entry)
DE Amino acid sequence of a human protein expressed in tumour cells.
KW Tumour cell; immunological disease; autoimmune disease; cancer;
OS infection.
PN Homo sapiens.
PN WO200131003-A1.
PD 03-MAY-2001.
PE 30-OCT-2000; 2000WO-FR03032.
PF 29-OCT-1999; 99FR-0013629.
PR (FABR ) FABRE MEDICAMENT SA PIERRE.
PA Delneste Y, Magistrelli G, Jeannin P, Bonnefoy J;
PI WPI: 2001-328651/34.
XX N-PSDB: AAF89774.
DR New nucleic acid, expressed in tumours and lymphoid tissue is useful for
PT Identifying agents for treating tumours and autoimmune disease
PS Claim 10; Page 60-63; 85bp; French.
XX
XX The present sequence represents a human protein expressed in tumour
XX cells. The polynucleotide is useful for screening cDNA/genomic DNA banks
XX and for cloning isolated DNA; identifying mutant forms of the gene that
XX encodes a human protein, where the mutations are associated with
XX abnormal gene expression, or promoters and regulators of the gene,
XX particularly for diagnosis; for recombinant expression and amplification; and
XX as antisense therapeutics. The tumour expressed protein is useful for
XX raising specific antibodies and to screen agents that modulate its
XX activity, bind to it or interact with it. These agents are potentially
XX useful for treatment or prevention of diseases associated with abnormal
XX expression/activity of the protein, particularly immunological diseases
XX (autoimmune diseases and cancer) or viral, bacterial, fungal or parasitic
XX infections.
SO Sequence 911 AA;
Query Match 90.9%; Score 5005; DB 22; Length 911;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 908; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 MAEPGHSHLSARVGRTERRIRPLMLLLMAGTAQVOTGTGPELHACKESYHEYYTA 60
DB 1 MAEPGHSHLSARVGRTERRIRPLMLLLMAGTAQVOTGTGPELHACKESYHEYYTA 60
OY 61 CDSTGSRMRVAVPHPTPGICTSLPDPVKGTECSFSCNAGEFLDMKDCSCPCAGRSYSLGT 120
DB 61 CDSTGSRMRVAVPHPTPGICTSLPDPVKGTECSFSCNAGEFLDMKDCSCPCAGRSYSLGT 120
OY 121 GIREDEMDLPHGFASLSANMELDLSAAESTGNTSSKWPVRGDIYAFNDECTATLMTA 180
DB 121 GIREDEMDLPHGFASLSANMELDLSAAESTGNTSSKWPVRGDIYAFNDECTATLMTA 180
OY 181 VNLKOSGTVNFEXYYPDSIIIFEEFVONDQCPNADSRMMKTTTEKMEFHSVELNRGN 240
DB 181 VNLKOSGTVNFEXYYPDSIIIFEEFVONDQCPNADSRMMKTTTEKMEFHSVELNRGN 240
OY 241 VLYWRTAFSVTKVPKPLVRLNIAITGVAYTSECFPCPKGTADKOGSSFCCLCPANSY 300
DB 241 VLYWRTAFSVTKVPKPLVRLNIAITGVAYTSECFPCPKGTADKOGSSFCCLCPANSY 300

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OY 301 SNKGETSCHODPDKYSKSSSCNVPRACDXTDKDYFYTHHACDANGETOIMYKAPKIC 360
DB 301 SNKGETSCHODPDKYSKSSSCNVPRACDXTDKDYFYTHHACDANGETOIMYKAPKIC 360
OY 361 SEDLEGAVKLAASGVKTHCPKPCNPGFKTNNSTQCPCPYGSSNGSDCTRCAPAGTPAVG 420
DB 361 SEDLEGAVKLAASGVKTHCPKPCNPGFKTNNSTQCPCPYGSSNGSDCTRCAPAGTPAVG 420
OY 421 FEYKMMNTLPNTMETVYLSGINFEYKGMTGMEVAGDHITAAASDNDPMILTLVYVGR 480
DB 421 FEYKMMNTLPNTMETVYLSGINFEYKGMTGMEVAGDHITAAASDNDPMILTLVYVGR 480
OY 481 PRQVMAADTEKKEVARITFEVETLCSVNCELYPMGVNSKRTNTPVETWKGSGKOSYTYI 540
DB 481 PRQVMAADTEKKEVARITFEVETLCSVNCELYPMGVNSKRTNTPVETWKGSGKOSYTYI 540
OY 541 IEENTTSFTWAFORTFEHASKRYNDVAKIYSINVTVMNGVASYCRPCALASDVGS 600
DB 541 IEENTTSFTWAFORTFEHASKRYNDVAKIYSINVTVMNGVASYCRPCALASDVGS 600
OY 601 SCTSCPAGYIYDRDSCGCHSCPNTILKAHOPYGAVCPGPGTKNNKIHSLCYNDCGF 660
DB 601 SCTSCPAGYIYDRDSCGCHSCPNTILKAHOPYGAVCPGPGTKNNKIHSLCYNDCGF 660
OY 661 SRMTPTFTFNYNSALANTYTLAGSPFTSKGLKTFHHTTSLCNGGRKMSVCTDNTD 720
DB 661 SRMTPTFTFNYNSALANTYTLAGSPFTSKGLKTFHHTTSLCNGGRKMSVCTDNTD 720
OY 721 LRPESESGFSKITAYVCOAVIIPPEVYKAGVSSOPVSLADLLIYVTDMLDGTTS 780
DB 721 LRPESESGFSKITAYVCOAVIIPPEVYKAGVSSOPVSLADLLIYVTDMLDGTTS 780
OY 781 PALFLESLGIDPVYEFRRSDVYQSCSGSTTIRVRCSPQKTPGSLLLPGTCSGDT 840
DB 781 PALFLESLGIDPVYEFRRSDVYQSCSGSTTIRVRCSPQKTPGSLLLPGTCSGDT 840
OY 841 CDGCFHFLMESAAACPLCSVADYHAIVSSCVAGIOKTTYWMBREKICSGSISLPEQRYT 900
DB 841 CDGCFHFLMESAAACPLCSVADYHAIVSSCVAGIOKTTYWMBREKICSGSISLPEQRYT 900
OY 901 ICKTIDFWLKY 911
DB 901 ICKTIDFWLKY 911

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RESULT 6
AAB83851
ID AAB83851 standard; Protein: 870 AA.
XX
AC AAB83851;
XX
DT 23-JUL-2001 (first entry)
XX
DE Amino acid sequence of a human protein expressed in tumour cells.
XX
KW Tumour cell; immunological disease; autoimmune disease; cancer;
XX
KW Infection.
XX
OS Homo sapiens.
XX
PN MO2001J1003-A1.
XX
PD 03-MAY-2001.
XX
PE 30-OCT-2000; 2000MO-FR03032.
XX
PR 29-OCT-1999; 99PR-0013629.
XX
PA (FABR ) FABRE MEDICAMENT SA PIERRE.
XX
PI Delneste Y, Magistrelli G, Jeannin P, Bonnefoy J;
XX
DR WPI; 2001-328651/34.

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DR N-PSDB: AAF89775.
XX
PT New nucleic acid, expressed in tumours and lymphoid tissue is useful for
PT Identifying agents for treating tumours and autoimmune disease
XX
PS Claim 10; Page 67-70; 85pp; French.
XX
CC The present sequence represents a human protein expressed in tumour
CC cells. The polynucleotide is useful for screening cDNA/genomic DNA banks
CC and for cloning isolated DNA; identifying mutant forms of the gene that
CC encodes a human protein, where the mutations are associated with
CC abnormal gene expression, or promoters and regulators of the gene,
CC particularly for diagnosis; for recombinant expression of the derived
CC protein; as probes and primers for detection and amplification; and
CC as antisense therapeutics. The tumour expressed protein is useful for
CC raising specific antibodies and to screen agents that modulate its
CC activity, bind to it or interact with it. These agents are potentially
CC useful for treatment or prevention of diseases associated with abnormal
CC expression/activity of the protein, particularly immunological diseases
CC (autoimmune diseases and cancer) or viral, bacterial, fungal or parasitic
CC infections.
XX
SQ Sequence 870 AA:
XX
Query Match 86.9%; Score 4784; DB 22; Length 870;
Best local Similarity 99.7%; Pred. No. 0;
Matches 867; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 42 TGBELHAKSESEHYEYACDSTGSRMRVAVPHRPGCLTSLPDPYKGECSFSCNAEFL 101
DB 1 TGBELHAKSESEHYEYACDSTGSRMRVAVPHRPGCLTSLPDPYKGECSFSCNAEFL 60
OY 102 DMKDQCKRCACGRSLGTGIRFDEWDELPHGFASLSANMELDASAESTGNCSSKWP 161
DB 61 DMKDQCKRCACGRSLGTGIRFDEWDELPHGFASLSANMELDASAESTGNCSSKWP 120
OY 162 RGDYIAFNTDECTATLAVNLKOSGTNFEYYPDSIIIFEEFVQNDQCPNADDSRW 221
DB 121 RGDYIAFNTDECTATLAVNLKOSGTNFEYYPDSIIIFEEFVQNDQCPNADDSRW 180
OY 222 KTEKGWGFHSVELRGNVLYWRTAFSVWTKVKKPVLVRLNIAITGVATSECFPCR 281
DB 181 KTEKGWGFHSVELRGNVLYWRTAFSVWTKVKKPVLVRLNIAITGVATSECFPCR 240
OY 282 TYADKQSSFCCLCPANSYKSGEHSCHODPDKYSKSSSCNVPRACDXTDKDYFYTH 341
DB 241 TYADKQSSFCCLCPANSYKSGEHSCHODPDKYSKSSSCNVPRACDXTDKDYFYTH 300
OY 342 CDANGETOIMYKAPKICSEDLGAVKLPASGVKTHCPKPCNPGFKTNNSTQCPCPYG 401
DB 301 CDANGETOIMYKAPKICSEDLGAVKLPASGVKTHCPKPCNPGFKTNNSTQCPCPYG 360
OY 402 YSNGSDCTRCAPAGTEPAVGFYKMMNTLPNTMETVYLSGINFEYKGMTGMEVAGDHIT 461
DB 361 YSNGSDCTRCAPAGTEPAVGFYKMMNTLPNTMETVYLSGINFEYKGMTGMEVAGDHIT 420
OY 462 AGASDNDPMILTLVYVGRPPQSVMAADTEKKEVARITFEVETLCSVNCELYPMGVNSRT 521
DB 421 AGASDNDPMILTLVYVGRPPQSVMAADTEKKEVARITFEVETLCSVNCELYPMGVNSRT 480
OY 522 NTPVETWKGSGKOSYTYIIEENTTSFTWAFORTFEHASKRYNDVAKIYSINVTVM 581
DB 481 NTPVETWKGSGKOSYTYIIEENTTSFTWAFORTFEHASKRYNDVAKIYSINVTVM 540
OY 582 NGVASYCRPCALASDVGSCTSPAGYIYDRDSCGCHSCPNTILKAHOPYGAVCPG 641
DB 541 NGVASYCRPCALASDVGSCTSPAGYIYDRDSCGCHSCPNTILKAHOPYGAVCPG 600
OY 642 GPGTKNNKIHSLCYNDCFTSRNTPFTFNYNSALANTYTLAGSPFTSKGLKTFHHTL 701
DB 601 GPGTKNNKIHSLCYNDCFTSRNTPFTFNYNSALANTYTLAGSPFTSKGLKTFHHTL 660
OY 702 SLGNGGRKMSVCTDNTDYLRIPESESGFSKITAYVCOAVIIPPEVYKAGVSSOPVS 761

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Db 661 SLGNGGRKMSGCTDNDVLDLRIPEGSEGSFSTITAYVQAVIIPPEVTGKAGVSOPPS 720
QY 762 LADRLIGVTTMTLDGITSIPAELFHELSIGIPDIFFYRSDNVTQSCSSGRSTTIRVCS 821
Db 721 LADRLIGVTTMTLDGITSIPAELFHELSIGIPDIFFYRSDNVTQSCSSGRSTTIRVCS 780
QY 822 POKTVPGSLLPPTCSDGTCDGCFNHFHLMESNAACPCLCSVADYNAIYSSCVAGIOKTIVV 881
Db 781 POKTVPGSLLPPTCSDGTCDGCFNHFHLMESNAACPCLCSVADYNAIYSSCVAGIOKTIVV 840
QY 882 WREPKLCSGIGISLPQORVITCKTIDFWLKV 911
Db 841 WREPKLCSGIGISLPQORVITCKTIDFWLKV 870

RESULT 7
AAB35328
ID AAB35328 standard; protein; 750 AA.
XX
AC AAB35328;
XX
DT 08-MAY-2001 (first entry)
XX
DE Human TR13 receptor protein SEQ ID NO: 2.
XX
KW Human; tumour necrosis factor receptor; TR13; TR14; infection;
KW cancer; autoimmune disease; allergy; inflammatory disease;
KW graft rejection; apoptosis; cardiovascular disease; aneurysm.
XX
OS Homo sapiens.
XX
PN W0200105834-A1.
XX
PD 25-JAN-2001.
XX
PF 14-JUL-2000; 2000MO-US19343.
XX
PR 16-JUL-1999; 99US-0144087.
PR 18-AUG-1999; 99US-0149450.
PR 20-AUG-1999; 99US-0149712.
PR 10-SEP-1999; 99US-0153089.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J, Young PE;
XX
DR WPI; 2001-112682/12.
DR N-PSDB; AAE27997.
XX
PT Nucleic acids encoding 2 human tumor necrosis factor receptor
PT polypeptides ((TR13) and (TR14)), useful for the prevention, diagnosis
PT and treatment of, e.g. cancers, acquired immune deficiency syndrome and
PT hypohidrotic ectodermal dysplasia -
XX
PS Claim 40; Page 369-372; 418pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC human tumour necrosis factor receptors TR13 and TR14. These sequences are
CC useful in the diagnosis and treatment of many diseases, including cancer,
CC autoimmune diseases, cardiovascular disorders, allergies,
CC neurodegenerative diseases, graft rejection, inflammation, aneurysms and
CC infections.
XX
SQ Sequence 750 AA;
XX
Query Match 70.3%; Score 3870; DB 22; Length 750;
Best Local Similarity 99.0%; Pred. No. 1.6e-293;
Matches 707; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 288 GSSFEKCLCPAASVKNKGTSCHOCDPDKYSEKSSSCNVPACTDKDYFYHTACDANCE 347
Db 37 GILFLOTLPSNYSNKGKETSCHQCDPKYSEKSSSCNVPACTDKDYFYHTACDANCE 96

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QY 348 TOLMYKMAKPKICSEDELEGAANKLPASGVKTHCPPCNPGFEKTNNSTQCOPCYGSGSYNGSD 407
Db 97 TOLMYKMAKPKICSEDELEGAANKLPASGVKTHCPPCNPGFEKTNNSTQCOPCYGSGSYNGSD 156
QY 408 CTRCPAGTEPVAAGFEYKWMNTLPTNMETTVLSGINFEEYKMTGMEVAGDHITTAAGASDN 467
Db 157 CTRCPAGTEPVAAGFEYKWMNTLPTNMETTVLSGINFEEYKMTGMEVAGDHITTAAGASDN 216
QY 468 DEMILTLVPGFRPQOSVMAOTENKEVARITFEVETLCSVNCLEYFVWGVNSRTNPEVT 527
Db 217 DEMILTLVPGFRPQOSVMAOTENKEVARITFEVETLCSVNCLEYFVWGVNSRTNPEVT 276
QY 528 WKSGSKGOSYTYITIEENTTSFTNAFQRTTFEASRKYNDVAKIYISINTNVNNGVASY 587
Db 277 WKSGSKGOSYTYITIEENTTSFTNAFQRTTFEASRKYNDVAKIYISINTNVNNGVASY 336
QY 588 CRPCALEASDVGSCTSCPAGIYIDRDSGTCHSCPNTILKAHOPYQVQACVPCGPGTKN 647
Db 337 CRPCALEASDVGSCTSCPAGIYIDRDSGTCHSCPNTILKAHOPYQVQACVPCGPGTKN 396
QY 648 NKIHSLCYNDCTFSRNTPTRTFNYSALANTVTLAGGSFTSKGLKYFHHFTLSLGNQ 707
Db 397 NKIHSLCYNDCTFSRNTPTRTFNYSALANTVTLAGGSFTSKGLKYFHHFTLSLGNQ 456
QY 708 GRKMSVCTDNTVTDLRIPEGSEGSFSTITAYVQAVIIPPEVTGKAGVSOPVSLADRLI 767
Db 457 GRKMSVCTDNTVTDLRIPEGSEGSFSTITAYVQAVIIPPEVTGKAGVSOPVSLADRLI 516
QY 768 GVTTDMTLDGITSIPAELFHELSIGIPDIFFYRSDNVTQSCSSGRSTTIRVCSPOKIVP 827
Db 517 GVTTDMTLDGITSIPAELFHELSIGIPDIFFYRSDNVTQSCSSGRSTTIRVCSPOKIVP 576
QY 828 GSLLPPTCSDGTCDGCFNHFHLMESNAACPCLCSVADYNAIYSSCVAGIOKTIVVWREPKL 887
Db 577 GSLLPPTCSDGTCDGCFNHFHLMESNAACPCLCSVADYNAIYSSCVAGIOKTIVVWREPKL 636
QY 888 CSGGISLPEQORVITCKTIDFWLKVISAGTCTAILTLVLCYFMKKNOKLEYXSKLVNN 947
Db 637 CSGGISLPEQORVITCKTIDFWLKVISAGTCTAILTLVLCYFMKKNOKLEYXSKLVNN 696
QY 948 ATIKKCDLPADSCAIMEGDEVEDDLFTSKNHSLSGNSHLPPRGLMDLTQCR 1001
Db 697 ATIKKCDLPADSCAIMEGDEVEDDLFTSKNHSLSGNSHLPPRGLMDLTQCR 750

RESULT 8
AAB70256
ID AAB70256 standard; protein; 1027 AA.
XX
AC AAB70256;
XX
DT 10-MAY-2001 (first entry)
XX
DE TR16-long receptor protein.
XX
KW TR16 receptor; tumour necrosis factor receptor superfamily;
KW apoptosis; inflammatory; cancer; immune; neurodegenerative.
XX
OS unidentified.
XX
PN W0200112671-A1.
XX
PD 22-FEB-2001.
XX
PF 10-AUG-2000; 2000MO-US21885.
XX
PR 12-AUG-1999; 99US-0148348.
PR 13-AUG-1999; 99US-0148683.
PR 13-AUG-1999; 99US-0148670.
PR 16-AUG-1999; 99US-0148758.
PR 17-AUG-1999; 99US-0149181.
PR 18-AUG-1999; 99US-0149453.

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PR 19-AUG-1999; 9905-0149498.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA Ruben SM, Young PE, Baker KP;  
 XX WPI; 2001-138754/14.  
 DR  
 XX  
 PT New nucleic acid molecule encoding a TR16 tumor necrosis factor  
 PT receptor polypeptide, useful for the diagnosis and treatment of cancer,  
 PT autoimmune disorders and cardiovascular diseases -  
 XX  
 PS Disclosure; Fig 4; 286pp; English.  
 CC  
 CC The present invention relates to a TR16 receptor (tumour necrosis  
 CC factor receptor superfamily). The invention is useful treating  
 CC diseases and disorders associated with the inhibited or increased  
 CC apoptosis. In particular inflammatory diseases, cancers, immune and  
 CC neurodegenerative disorders may be treated.  
 XX  
 SQ Sequence 1027 AA;

Query Match 54.2%; Score 2982.5; DB 22; Length 1027;  
 Best Local Similarity 53.6%; Pred. No. 1.7e-225;  
 Matches 530; Conservative 168; Mismatches 270; Indels 21; Gaps 11;

OY 15 RGRTERRIIPR---LMRL-----LMAAGTAFOYGTGPELAAKSEHYHYETAADSTGSR 67  
 DB 23 RGRSPSPSPAMICWALAGCOAAMAG--DLPSSSSRPLPPCQKDYHFEYTCDDSSGSR 79  
 OY 68 WRVAVPHTPGICTSLPDPVKGTSCSFSCNAGEFLDMKDKOCPCAREGRYSLGIGIRFDEW 127  
 DB 80 WRVAVPNSAVVDCSGLPDPVRGKECTFCASGEYIEKKNQVCSKCGREYSLGSGIGIRFDEW 139  
 OY 128 DELPAGFASLSANNELDSDAAS-TCNCTSSKVPYRGDIYAFNTDCTATLMAVNLKOS 186  
 DB 140 DELPAGFSNLTAFMDYVAGPDSRPDGCNNNSWIPRGNTIESNRDCTVSLIYAVHLKKS 199  
 OY 187 GTVNFEEYYPDSIIFFEFYQNDQCP-NADDSRMKKTTEKG-WEHSHSELNKGNNVLYW 244  
 DB 200 GYVFEFYQYDNNIFFEYFIONQCEMDYTTKWKYKLDNGEMGSHSLASGNTILYW 259  
 OY 245 RTTAFSVWTKVPRVLYRNATIGVATSECFPCPGIYADKOGSSFFCLCPANSYSNGK 304  
 DB 260 RTTGILMGSAVRPVLYKNTTIGVATSECFPCPGIYADKOGSSFFCLCPANSYSNGK 319  
 OY 305 ETSCHOC-DEPKYSEKSSCNRPACTDKDYFTTTADANGETOLMKAKPRICSED 363  
 DB 320 AKECIRCKDSDQS--GSSECTERPECTTKDYFQIHTPCDEGKTQIMWKIEPKICRED 377  
 OY 364 LBGAVLPLASGVKTHCPGCPNPGFEFTKNNSTQCPYGSYSNGS-DCTRCPAGTEPAVGE 422  
 DB 378 LQDAIRLPPSGEKKDCPCNPGFYNNSSSCHPCPGIFSDOTKRCRCRCPAGTEPALGE 437  
 OY 423 YKMMNTLPNNMETVLSGTFEYKMGTEVAAGDHIYTAAGASDNDENILTLVVGFRPP 482  
 DB 438 YKMMNTLPNNMETVLSGTFEYKMGTEVAAGDHIYTAAGASDNDENILTLVVGFRPP 497  
 OY 483 QSVAMADTENKEVARTTFEFTLCVNCLELYPMVGNSTNTPVETWNGSKGOSYITIE 542  
 DB 498 TS-MGATGSELGRTTFEFTLCVNCLELYPMVGNSTNTPVETWNGSKGOSYITIE 556  
 OY 543 ENTTSFTWAPORTTFHASKRYTNDVAKIYSINVTVMNGVASYCRPCALASDVSSC 602  
 DB 557 KNAITTFWAPORTTFHASKRYTNDVAKIYSINVTVMNGVASYCRPCALASDVSSC 616  
 OY 603 TSPAGYYIDRSGTCHSCPNTTILKAHOPGVAGVPCPCPKRNNKTHSLCINDCTFSR 662  
 DB 617 VPCPGHYIEKETNOCKKCPDYTLISHOYVKGACIPCGPSSKNNDHVSVCDFEYH 676  
 OY 663 NTPRTFYNNSALANTVYTLAGSPSTSKILYFHHFTLSLCNGQGRKMSVCTDVTDLR 722  
 DB 677 EKENQILHYDESNLSVSGILMNGPSFTSKGTKEFHFNISLCSGHEKKMALCTNNITDFT 736

OY 723 IPE---GEGSEKSIITAYVQAVIIPPEVTGYKAGVSSQVPLADRLIGVTTDMTLDGIT 779  
 DB 737 VKELVAGSDDTMLVGAFCOSTIIPSEKSGFRMASSOSIILADTFIGVFEYETLLKMIN 796  
 OY 780 SPAELHLESIGIPDIVIFFEYRNDVYQSCSSGRSTTIRVCSPOKTVGSGILLPRTGSDG 839  
 DB 797 IKEDMPEVPVTSQIPDVHFEYKSSSTATTSCINGRSTAVAKMRPKFGAGVLSVPSKCPAG 856  
 OY 840 TCGGCPNHFHLEMSAACPLCSADYADHAIYSCVAGIQTKTYVMREPKLCSGISLPEDRV 899  
 DB 857 TCGGCTFFELWESAECPLCTEDHDEHEIGACRGEFETLYVMNEPKVICIGISLPKEL 916  
 OY 900 TICKTIDFWLKVISAGTCTAILTLVLCYFPKKRQKLEYKSLYNNMATLKDDCLPAD 939  
 DB 917 ANCEYVDFWLKVGAGVAFATLVALCYTRKKRQKLEYKSLYNNMATLKDDCLPAD 976  
 OY 960 SCALMEGEVEEDLFTSKNHSLSGRSNHL 988  
 DB 977 SCALMEGEVEEDLFTSKNHSLSGRSNHL 1005

RESULT 9  
 AAB70255  
 ID AAB70255 standard; protein; 963 AA.

XX AAB70255;  
 AC  
 XX 10-MAY-2001 (first entry)  
 DT  
 XX  
 DE TR16-short receptor protein.  
 XX  
 KW TR16 receptor; tumour necrosis factor receptor superfamily;  
 KW apoptosis; inflammatory; cancer; immune; neurodegenerative.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112671-A1.  
 PD  
 XX 22-FEB-2001.  
 PF  
 XX 10-AUG-2000; 2000WO-US21885.  
 PR 12-AUG-1999; 9905-0148348.  
 PR 13-AUG-1999; 9905-0148683.  
 PR 16-AUG-1999; 9905-0148870.  
 PR 17-AUG-1999; 9905-0148758.  
 PR 18-AUG-1999; 9905-0149181.  
 PR 19-AUG-1999; 9905-0149453.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA Ruben SM, Young PE, Baker KP;  
 PI WPI; 2001-138754/14.  
 DR  
 XX  
 PT New nucleic acid molecule encoding a TR16 tumor necrosis factor  
 PT receptor polypeptide, useful for the diagnosis and treatment of cancer,  
 PT autoimmune disorders and cardiovascular diseases -  
 XX  
 PS Claim 1; Fig 1; 286pp; English.  
 CC  
 CC The present invention relates to a TR16 receptor (tumour necrosis  
 CC factor receptor superfamily). The invention is useful treating  
 CC diseases and disorders associated with the inhibited or increased  
 CC apoptosis. In particular inflammatory diseases, cancers, immune and  
 CC neurodegenerative disorders may be treated.  
 XX  
 SQ Sequence 963 AA;

Query Match 51.1%; Score 2815.5; DB 22; Length 963;  
 Best Local Similarity 52.8%; Pred. No. 2.2e-212;



Matches	501; Conservative	161; Mismatches	261; Indels	25; Gaps	12;
OY	15 RGRTERIR---LMRL---LLMAGTAFQVYOGTGPFLHACKSESEVYETXACTDSTGR	67			
DB	23 RGRSPWSPAMICCMALACQAMAG---DLFSSSSRLPPCQEKEDYFEFTECDSSGR	79			
OY	68 WRAVAHPHTGLTSLPDPKGTCECSFSCNAGEFLDMKQDQSKPCAEGRYSIGTGIRPEW	127			
DB	80 WRAVAIRSAVDCGLPDPVRKCECTSCASGEYLEKMKNOVCSKCEGTSLSGSKPEW	139			
OY	128 DELPHGASISANMELDDSAES--TGNCSSKRVPRGDYIAFNTDECTATIMAYANLKS	186			
DB	140 DELPAGESNATFMDTVVGVSPDRDGNSSWIPRGNTIESNRDDCTSLIYANHLKS	199			
OY	187 GTVAFEEYDDSSIIFFEFVQNDQOP--NADDSRMKKTTEG--WEFSEYELRNKNVLYW	244			
DB	200 GYVEFEYQYDNNITFEFFIIONDQCEMDTTDKVKYKLDNGEMGSHSVMKSGTNILYW	259			
OY	245 RTTAFSVTKVPKVLVRLNATITGVAITSFPCFPCGTADKQSSFCGLCPANSYNGK	304			
DB	260 RTTGILMSKAVKVLKNTITIEVATSECFCKPFTSNKGSFNCQVCRNTYSEK	319			
OY	305 ETSCHOC--DPRKSEKSSSCNVBPACTDKDYTYHTACDANGETOLMTAKPKTCSGD	363			
DB	320 AKECIRCKDQDSQFS--GSSECTERPTCTMDYQIHTPCDEEGKTQIMYKWIETPKICRD	377			
OY	364 LEGAVKLPAAGVKTCHPCPNDFEFTKNNSTCQPCPYGSYNGS--DCRCPAGTEPAVGE	422			
DB	378 LTDAIRLPPESEKCKPCPCPNDFPNNGSSSCPCPPTSGTKCKPCACAGTEPALGE	437			
OY	423 YKMMNLTLPNNMETVLSINFEYKMGMEVAGDHIYTAGASDNDMLTLVVGRRP	482			
DB	438 YKMMNVLGNMTSCFVNGNSKCDGMNEVAGDHIOSGASDNDLILNLHPGKRP	497			
OY	483 QSMADTENKEVARITFEVETLCYNCLIEPMGVNSTNTPVETMGSKOKOSTYIIE	542			
DB	498 TS--MTGATSELRITFEVETLCYADCVLYFWDINRSTNVESWGSTRKOKAYTHIF	556			
OY	543 ENTTTFETWAPQRTFHEASRKYTNDVAKIYSINVTNMGVASYRCPCALEASDVSSC	602			
DB	557 KNATFEFTWAFORTNOGONRPFINDMKIYITATNADGVAASCRACALGSESSSC	616			
OY	603 TSCPAGYIDRDSGTCHSCPNTILKAHOPYVOACVCGPCTKNNKTHSICYNDCPFSR	662			
DB	617 VPCPGHYIEKFNQCKECPDPTYLISHQVYGEKACIPCGPESKNNQDHVCYSDCFYH	676			
OY	663 NTPTPTFNYSALANTVTLAGSPFTSKGLYFHHFTLSLQNGGRKMSVCTDNDLR	722			
DB	677 EKENQILHDFNSLSVSGSLMNGPFTSKGTGFHFENISLCSGHEKMKALCTNNITDFT	736			
OY	723 IPE---GEGFSKSIYAYCOAVIIPPEVYGYAGYSSOPVSLADRLIGVTTDMTLDGIT	779			
DB	737 VKEIVASDDYTNLGVAFQCOSTIIPSESGFRAALSSQIILADFFIYVETTLKNN	796			
OY	780 SPALFHLBSLGPIDVIEFRSNDVQSCSSGRSTIRVCSPOKTPVPSLLPGTCSDG	839			
DB	797 IKEMFEPVPSQIDPVIEFKTSNATISCTINGSTAVKMKCNPTKAGAYISVPSKCPAG	856			
OY	840 TDCGNEHFLWESAACPLCSVADYDAIYSSCAVAGIOKTYVVRKPLSGSGISLEPQY	899			
DB	857 TCDGTFEFLWESAACPLCTEHDHFEIEGCKRGFOETLYVNNRPMWCKTSGISLEPQY	916			
OY	900 TICTKIDFWLKVAGISAGCTAILTLVLCYFWKKNQKYLEYKSKLVNN	947			
DB	917 ATCEIVDFWLKVAGVGAFTAVLVALTLCTYWKKNQKK---KTIIN	960			

RESULT 10  
AA59972  
ID AA59972 standard; Protein: 495 AA.  
XX  
AC  
AY59972;  
XX

DT	31-JAN-2000 (first entry)
XX	
DE	Human endometrium tumour EST encoded protein 32.
XX	
KW	Endometrium; human; tumour; cancer; anticancer; cytostatic; EST;
KW	treatment; uterine; gene therapy; expressed sequence tag.
XX	
OS	Homo sapiens.
XX	
PN	DE19817948-A1.
XX	
PD	21-OCT-1999.
XX	
PF	17-APR-1998; 98DE-1017948.
XX	
PR	17-APR-1998; 98DE-1017948.
XX	
PA	(META-) METAGEN GES GENOMFORSCHUNG MBH.
XX	
PI	Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
XX	
DR	WPI; 1999-591957/51.
XX	
PT	New nucleic acid sequences expressed in uterine cancer tissues, and
PT	derived polypeptides, for treatment of uterine and endometrial cancer
XX	and identification of therapeutic agents
XX	
PS	Claim 23; Page 287; 444pp; German.
XX	
CC	This invention describes novel human nucleic acid (cDNA) sequences (A),
CC	that are highly expressed in uterine tumour tissue and which have
CC	anticancer and cytostatic activity. (A) are used (i) for recombinant
CC	expression of polypeptides (B) and (ii) to isolate complete genes. (B)
CC	are used (i) to identify agents suitable for treatment of uterine or
CC	endometrial cancer; (ii) directly for treating these forms of cancer
CC	(including expression from gene therapy vectors) and (iii) for
CC	generation of specific antibodies. (A) are identified by assembling ESTs
CC	(expressed sequence tags) from a particular tissue type before comparison
CC	of expression patterns. This allows a significantly longer fragment of
CC	the gene to be revealed, so should reduce the number of failures
CC	associated with the fact that ESTs from different libraries may represent
CC	different parts of the same unknown gene, distorting the estimated
CC	frequency of occurrence in a particular tissue. AA59941-Y60328 represent
CC	protein fragments encoded by the human endometrium tumour cDNA library
CC	derived EST fragments represented in AA41981-742121.
XX	
SO	Sequence 495 AA:
XX	
Query Match	45.2%; Score 2491; DB 20; Length 495;
Best Local Similarity	98.9%; Pred. No. 2.9e-187;
Matches 461; Conservative	1; Mismatches 4; Indels 0; Gaps 0;
OY	519 SRTNTPVETWKSCKKOSTYIIEENTTSFMAFQRTFHEASRKYTNDVAKIYSINVT 578
DB	1 SRTNTPVETWKSCKKOSTYIIEENTTSFMAFQRTFHEASRKYTNDVAKIYSINVT 60
OY	579 NVNMGVASYRCPCALEASDVSSCTSCPAGYIDRDSGTCHSCPNTILKAHOPYVOAC 638
DB	61 NVNMGVASYRCPCALEASDVSSCTSCPAGYIDRDSGTCHSCPNTILKAHOPYVOAC 120
OY	639 VPCPGTKNNKTHSLCTNDCTFSRNPPTFFNNFNSALANTVTLAGGSPFTSKGLKTYHH 698
DB	121 VPCPGTKNNKTHSLCTNDCTFSRNPPTFFNNFNSALANTVTLAGGSPFTSKGLKTYHH 180
OY	699 FTLSLQNGGRKMSVCTDNDLIRIPGSGFSKSIYAYCOAVIIPPEVYGYAGYSSQ 758
DB	181 FTLSLQNGGRKMSVCTDNDLIRIPGSGFSKSIYAYCOAVIIPPEVYGYAGYSSQ 240
OY	759 PVSILADRLIGVTTDMTLDGITSPALFHLBSLGPIDVIEFRSNDVQSCSSGRSTIRV 818
DB	241 PVSILADRLIGVTTDMTLDGITSPALFHLBSLGPIDVIEFRSNDVQSCSSGRSTIRV 300

QY 819 KCSPOKTVPGSLLPGETSGDTCDCNPFHFLMESAAACPLCSVADYHAIVSSCVAGIOKT 878  
 DB 301 KCSPOKTVPGSLLPGETSGDTCDCNPFHFLMESAAACPLCSVADYHAIVSSCVAGIOKT 360  
 QY 879 TVWMEPEPLCSGGISLPQRYATICTIDFWLKVGISAGTCTAILLYLTCTYFMKKNOKE 938  
 DB 361 TVWMEPEPLCSGGISLPQRYATICTIDFWLKVGISAGTCTAILLYLTCTYFMKKNOKE 420  
 QY 939 YKSKLVNATLKDODLPAAADSCAIMGEDEVEDLLFTSKNHSIGR 984  
 DB 421 YKSKLVNATLKDODLPAAADSCAIMGEDEVEDLLFTSKNHSIGR 466

## RESULT 11

ID AAB83853 standard; Protein; 383 AA.  
 AC AAB83853;  
 DT 23-JUL-2001 (first entry)  
 DE Amino acid sequence of a human protein expressed in tumour cells.  
 KW Tumour cell; immunological disease; autoimmune disease; cancer;  
 KW infection.  
 OS Homo sapiens.  
 PN WO200131003-A1.  
 PD 03-MAY-2001.  
 PF 30-OCT-2000; 2000MO-FR03032.  
 PR 29-OCT-1999; 99FR-0013629.  
 PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
 PI Delneste Y, Magistrelli G, Jeannin P, Bonnefoy J;  
 DR WPI: 2001-328651/34.  
 DR N-PSDB: AAF89777.  
 PT New nucleic acid, expressed in tumours and lymphoid tissue is useful for  
 PT identifying agents for treating tumours and autoimmune disease  
 Claim 10; Page 74-75; 85pp; French.

The present sequence represents a human protein expressed in tumour cells. The polynucleotide is useful for screening cDNA/genomic DNA banks and for cloning isolated DNA; identifying mutant forms of the gene that encodes a human protein, where the mutations are associated with abnormal gene expression, or promoters and regulators of the gene, particularly for diagnosis; for recombinant expression of the gene, protein; as probes and primers for detection and amplification; and as antisense therapeutics. The tumour expressed protein is useful for activity, bind to it or interact with it. These agents are potentially useful for treatment or prevention of diseases associated with abnormal expression/activity of the protein, particularly immunological diseases (autoimmune diseases and cancer) or viral, bacterial, fungal or parasitic infections.

Sequence 383 AA.

Query Match 38.5%; Score 2119; DB 22; Length 383;  
 Best Local Similarity 99.5%; Pred. No. 3.7e-158;  
 Matches 381; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 136 SISANNEILDSDAESTGNGCTSSKWPREDYIAFNTDECTATLMAVNLKOSGTVNFEEY 195  
 DB 1 SISANNEILDSDAESTGNGCTSSKWPREDYIAFNTDECTATLMAVNLKOSGTVNFEEY 60

QY 196 PSSIIIEEFYVQNOCCQPNADDSRMKTTTEKGEFHSVELNRGNVLYMRTAFSVMTKY 255  
 DB 61 PSSIIIEEFYVQNOCCQPNADDSRMKTTTEKGEFHSVELNRGNVLYMRTAFSVMTKY 120  
 QY 256 PKPVLVNRNIAITGAATYSECEPCPKGTADKQSSPFCKLCPASYSNKGTSCHQCDPK 315  
 DB 121 PKPVLVNRNIAITGAATYSECEPCPKGTADKQSSPFCKLCPASYSNKGTSCHQCDPK 180  
 QY 316 YSEKSSSCNRPACTKDYFYHTACDANGETOLMYKNAKPKICSEDEGAVKLPASGV 375  
 DB 181 YSEKSSSCNRPACTKDYFYHTACDANGETOLMYKNAKPKICSEDEGAVKLPASGV 240  
 QY 376 KTHCPNCPGFFFTNNSTOCPCRYGSYNSDCTRCPCAGTEPAVGFEYKMMATLPTNMT 435  
 DB 241 KTHCPNCPGFFFTNNSTOCPCRYGSYNSDCTRCPCAGTEPAVGFEYKMMATLPTNMT 300  
 QY 436 TVLSGTFEYKMGTVGEVADHITYTAAGASDNDFMILLVVGFRPPQSVNADTEKRYA 495  
 DB 301 TVLSGTFEYKMGTVGEVADHITYTAAGASDNDFMILLVVGFRPPQSVNADTEKRYA 360  
 QY 496 RITFEFETLCSVNCLEXYFMVGVN 518  
 DB 361 RITFEFETLCSVNCLEXYFMVGVN 383

## RESULT 12

ID AAB85768 standard; Protein; 372 AA.  
 AC AAB85768;  
 DT 29-OCT-2001 (first entry)

DE Human seven-transmembrane protein 50288 sequence.

seven-transmembrane protein; G-protein coupled receptor; GPCR; human;  
 17724; 50288; 31945; antiinflammatory; analgesic; cytostatic; virucide;  
 hepatotropic; immunosuppressive; gynecological; neuroprotective;  
 anti-HIV; immunostimulant; dermatological; antiatherosclerotic; candidant;  
 antianemic; antiParkinsonian; nephrotoxic; antithyroid; hemostatic;  
 cerebroprotective; osteopathic; analgesic; gene therapy; nootropic.

OS Homo sapiens.  
 PN WO200159117-A2.  
 PD 16-AUG-2001.

PF 12-FEB-2001; 2001MO-US04536.  
 PR 11-FEB-2000; 2000US-0182061.

PA (MILL-) MILLENNIUM PHARM INC.  
 PI Glucksmann MA, Silos-Santiago I;  
 DR WPI: 2001-514670/56.  
 DR N-PSDB: AAH76195, AAH76196.

PT New seven-transmembrane protein/G-protein coupled receptor polypeptides  
 PT and polynucleotides for diagnosing, treating seven-transmembrane  
 PT protein/receptor-related disorders and to identify modulators of  
 PT therapeutic use

Claim 8; Page 139-141; 144pp; English.

The invention provides isolated seven-transmembrane protein/G-protein coupled receptor polypeptides selected from 17724, 50288, 31945 proteins. Modulators of the polypeptides can be identified using a competition binding assay or an assay for receptor-mediated signal transduction. The polypeptides and polynucleotides are useful as reagents or targets in seven-transmembrane protein/receptor assays applicable to treatment and

diagnosis of seven-transmembrane protein/receptor-mediated disorders (see AAB76191 for a detailed description of the various disorders that can be treated or diagnosed using the polypeptides). The polynucleotides are useful to detect mutations in genes and gene expression products such as cDNA, as antisense constructs to control gene expression and for chromosome identification. The present sequence represents the human seven transmembrane protein 50288 sequence.

Sequence 372 AA:

Query Match 32.0%; Score 1761.5; DB 22; Length 372;

Best Local Similarity 96.7%; Pred. No. 4.8e-130; Mismatches 6; Indels 3; Gaps 1;

Matches 318; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

1 MAEPGSHLSARVGRTERIPRLMLLWAGTAFOYTGTEGFLHACKSEHYETA 60

1 MAEPGSHLSARVGRTERIPRLMLLWAGTAFOYTGTEGFLHACKSEHYETA 60

61 CDSTGSRMVAVPHPTGLCTSLPDPVKGTECSFSCNAGEFLDMKQSCPCAEGRYSIGT 120

61 CDSTGSRMVAVPHPTGLCTSLPDPVKGTECSFSCNAGEFLDMKQSCPCAEGRYSIGT 120

121 GIPFDEDELPHGFASLSANMELDLSAESTGCTSSKWPBGDIATNTDECTATLMYA 180

121 GIPFDEDELPHGFASLSANMELDLSAESTGCTSSKWPBGDIATNTDECTATLMYA 180

121 GIPFDEDELPHGFASLSANMELDLSAESTGCTSSKWPBGDIATNTDECTATLMYA 180

181 VNKQSGTVNFEYYPDSSTIFFEYFVQNDCCPNADDSKMKTKRGMFHSVELNRGN 240

181 VNKQSGTVNFEYYPDSSTIFFEYFVQNDCCPNADDSKMKTKRGMFHSVELNRGN 240

241 VLYRTAFSWTKKPKPVLVRLNIAITGVAYTSECPKPGIYADKQSSFCFKLPANSY 300

241 VLYRTAFSWTKKPKPVLVRLNIAITGVAYTSECPKPGIYADKQSSFCFKLPANSY 300

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

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301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

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301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

301 SNKGETSCHOCDDPKYS---EKSSSCNV 326

Polynucleotides encoding SECX proteins useful for treating disease characterized by an aberrant level of cell proliferation and/or differentiation like cancer or immune associated disorders -

Claim 1; Fig 10; 132pp; English.

The invention relates to human SECX polypeptides and polynucleotides encoding them. The SECX polypeptides can be expressed by standard recombinant methodology. The SECX polypeptides are useful for treating or preventing a SECX-associated disorder. The invention is useful in screening assays; detection assays (e.g. chromosomal mapping, cell and tissue typing, forensic biology); predictive medicine (diagnostic assays, prognosis assays, monitoring clinical trials, and pharmacogenomics); and methods of treatment (e.g. therapeutic and prophylactic), especially disorders characterized by aberrant cell proliferation and/or differentiation like cancer or immune associated disorders or gestational disease. The present sequence represents a SEC10 protein.

Sequence 464 AA:

Query Match 26.3%; Score 1448; DB 22; Length 464;

Best Local Similarity 56.1%; Pred. No. 3.1e-105; Mismatches 122; Indels 6; Gaps 6;

Matches 257; Conservative 73; Mismatches 122; Indels 6; Gaps 6;

1 MKDQSCPCAEGRYSIGTGIRFDEDELPHGFASLSANMELDLSAESTGCTSSKWP 161

1 MKDQSCPCAEGRYSIGTGIRFDEDELPHGFASLSANMELDLSAESTGCTSSKWP 161

162 RGDYLAETDECTATLMYANVKQSGTVNFEYYPDSSTIFFEYFVQNDCCPNADDSRW 220

162 RGDYLAETDECTATLMYANVKQSGTVNFEYYPDSSTIFFEYFVQNDCCPNADDSRW 220

61 RGVNIESNRDCVSLIYAVHLKSGYFEEYQVONNIFEFEEFQNDCCQEMDTTQKW 120

61 RGVNIESNRDCVSLIYAVHLKSGYFEEYQVONNIFEFEEFQNDCCQEMDTTQKW 120

221 MKTEKG-WEFHSEYELNRGNVLYWRTAFSVTKPKVYLVRLNIAITGVAYTSCFPCK 279

221 MKTEKG-WEFHSEYELNRGNVLYWRTAFSVTKPKVYLVRLNIAITGVAYTSCFPCK 279

121 VKLTDNEMGSHSVMKSGTNIILYMTTGLIMSKAVKLVKNTIETVATSECFPK 180

121 VKLTDNEMGSHSVMKSGTNIILYMTTGLIMSKAVKLVKNTIETVATSECFPK 180

280 PGTAYADKQSSFCFKLPANSYSNKGETSCHOC-DPPKYSSEKSSSCNVBPACTDKDYFT 338

280 PGTAYADKQSSFCFKLPANSYSNKGETSCHOC-DPPKYSSEKSSSCNVBPACTDKDYFT 338

181 PGTFENKRGSPFCVCPRNITSEKAKCEKRCDDDSFSESSSECTERRPCTTKDYFOI 240

181 PGTFENKRGSPFCVCPRNITSEKAKCEKRCDDDSFSESSSECTERRPCTTKDYFOI 240

339 HTACDANGETOLMYKMAKPKICSEDLGAVKLPASGVKTHCPGCPNGEFTNNSTOCP 398

339 HTACDANGETOLMYKMAKPKICSEDLGAVKLPASGVKTHCPGCPNGEFTNNSTOCP 398

241 HTPCDEBKQTQIMKWIPEKICREDLDAIRLPSSGKKCPGCPNGEFTNNSTOCP 300

241 HTPCDEBKQTQIMKWIPEKICREDLDAIRLPSSGKKCPGCPNGEFTNNSTOCP 300

399 YGSYSNGS-DCTRCPCAGTEPAVGEYKWMNTLPNTMETVLSGINEYKMTGMEVAGDH 457

399 YGSYSNGS-DCTRCPCAGTEPAVGEYKWMNTLPNTMETVLSGINEYKMTGMEVAGDH 457

301 PGTFSDGTREKRCPCAGTEPAVGEYKWMNTLPNTMETVLSGINEYKMTGMEVAGDH 360

301 PGTFSDGTREKRCPCAGTEPAVGEYKWMNTLPNTMETVLSGINEYKMTGMEVAGDH 360

458 IYTAGASDNDPMILTVVPGFRPOSVMADTENKEVARITFVEETLCVSNCELYPMVGV 517

458 IYTAGASDNDPMILTVVPGFRPOSVMADTENKEVARITFVEETLCVSNCELYPMVGV 517

518 NSRNTPYETWKSGSKGOSTYIIEENTTSFTNAFOR 555

518 NSRNTPYETWKSGSKGOSTYIIEENTTSFTNAFOR 555

361 IOSGAGSDNDVLIILNHPGRKPTTS-MTGATGSELRITFVEETLCVSNCELYPMVGV 419

361 IOSGAGSDNDVLIILNHPGRKPTTS-MTGATGSELRITFVEETLCVSNCELYPMVGV 419

420 NRKSTNVESMGTRKQAYTHIIFKNATFTTQICPR 457

420 NRKSTNVESMGTRKQAYTHIIFKNATFTTQICPR 457

420 NRKSTNVESMGTRKQAYTHIIFKNATFTTQICPR 457

420 NRKSTNVESMGTRKQAYTHIIFKNATFTTQICPR 457

420 NRKSTNVESMGTRKQAYTHIIFKNATFTTQICPR 457

420 NRKSTNVESMGTRKQAYTHIIFKNATFTTQICPR 457

420 NRKSTNVESMGTRKQAYTHIIFKNATFTTQICPR 457

420 NRKSTNVESMGTRKQAYTHIIFKNATFTTQICPR 457

420 NRKSTNVESMGTRKQAYTHIIFKNATFTTQICPR 457

XX WO200078802-A2.  
 XX 28-DEC-2000.  
 XX 23-JUN-2000; 2000WO-US17328.  
 XX 23-JUN-1999; 99US-0140584.  
 XX 20-JUL-1999; 99US-0144722.  
 XX 16-SEP-1999; 99US-0154520.  
 XX 22-JUN-2000; 2000US-0604286.  
 XX (CURA-) CURAGEN CORP.  
 XX  
 PI Shimkets RA, Fernandes E, Vernet C, Yang M, Boldog FL;  
 PI Hermann JL;  
 XX  
 DR MPI; 2001-071385/08.  
 DR N-PSDB; AAC84886.  
 XX  
 PT Polynucleotides encoding SECX proteins useful for treating disease  
 PT characterized by an aberrant level of cell proliferation and/or  
 XX differentiation like cancer or immune associated disorders.  
 XX  
 PS Claim 1; Fig 6; 132pp; English.  
 XX  
 CC The invention relates to human SECX polypeptides and polynucleotides  
 CC encoding them. The SECX polypeptides can be expressed by standard  
 CC recombinant methodology. The SECX polypeptides are useful for treating  
 CC or preventing a SECX-associated disorder. The invention is useful in  
 CC screening assays; detection assays (e.g. chromosomal mapping, cell and  
 CC tissue typing, forensic biology); predictive medicine (diagnostic assays,  
 CC prognostic assays, monitoring clinical trials, and pharmacogenomics); and  
 CC methods of treatment (e.g. therapeutic and prophylactic), especially  
 CC disorders characterized by aberrant cell proliferation and/or  
 CC differentiation like cancer or immune associated disorders or gestational  
 CC disease. The present sequence represents a SEC5 protein.  
 CC  
 XX  
 SO Sequence 411 AA;  
 Query Match 23.7%; Score 1307.5; DB 22; Length 411;  
 Best Local Similarity 57.3%; Pred. No. 3e-94;  
 Matches 231; Conservative 62; Mismatches 105; Indels 5; Gaps 5;  
 QY 157 SKWPRQDYAFNTDECTATIMYAVNLKSGTYNFEYDDSIIFEPVQDQOP-NA 215  
 DB 3 SSMIPRCNTYIESNRDDCTVSLIYAVHLKSGYVEFYQVYNNIFFEFTQNDQOQEMDT 62  
 QY 216 DDSRMKTTKKG-WEPHSEVLNNGNVLKRTTASVWTKVPRVLYRNIAITGVAATSE 274  
 DB 63 TTRKWKVLIDNGEMGSHVWLKSGTILYRTGILMGSKAVKPYLVKNITIEGVAATSE 122  
 QY 275 CFPCKRGTYADKOGSSFCFLCPANSYNSKGETSCHOC-DPDKYSKSSSCNVRACIDK 333  
 DB 123 CFPCKRGTFESNKRPGFNCQVCPRNTYSEKGAECIRCKDDSOFSSEGSSECTERPCYTK 182  
 QY 334 DYFTHTADANGEOIAMKAKPKICSEDDLEGAVALPASGVKHCPCNCGFEKTNST 393  
 DB 183 DYQHTPCDEBERKTOIMKWEIKICREDLDLDAIRLPSEKKKCCPCNGCFVNNSSS 242  
 QY 394 COPCPYGSYNSG-DCTRCPAGTEPAVGEFEKMMNTLPTNNETTVLSGINFERYGMGME 452  
 DB 243 CHPCPGTFSDDTKRCRCBPAGTEPALOFEYKMMNVLPGNKTKSCFVNGNSKCGMNGWE 302  
 QY 453 VAGDHHTYTAGASDNDMILLVLVDEGFRPPQSVADTENKEVARITFEFTLCSVNCLEY 512  
 DB 303 VAGDHHTYTAGASDNDMILLVLVDEGFRPPQSVADTENKEVARITFEFTLCSVNCLEY 512  
 QY 513 FAVGVNSRTNTPVETWMSKSGKOSYTYIIEENTTSFTMAFOR 555  
 DB 362 FAVGVNSRTNTPVETWMSKSGKOSYTYIIEENTTSFTMAFOR 555  
 DB 362 FAVGVNSRTNTPVETWMSKSGKOSYTYIIEENTTSFTMAFOR 555

RESULT 15  
 AAB83852  
 ID AAB83852 standard; Protein; 209 AA.  
 XX  
 AC AAB83852;  
 XX  
 DT 23-JUL-2001 (first entry)  
 XX  
 DE Amino acid sequence of a human protein expressed in tumour cells.  
 XX  
 KW Tumour cell; Immunological disease; autoimmune disease; cancer;  
 KW Infection.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200131003-A1.  
 XX  
 PD 03-MAY-2001.  
 XX  
 PF 30-OCT-2000; 2000WO-FR03032.  
 XX  
 PR 29-OCT-1999; 99FR-0013629.  
 XX  
 PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
 XX  
 PI Delneste Y, Magistrelli G, Jeannin P, Bonnefoy J;  
 XX  
 DR MPI; 2001-328651/34.  
 DR N-PSDB; AAF89776.  
 XX  
 PT New nucleic acid, expressed in tumours and lymphoid tissue is useful for  
 PT identifying agents for treating tumours and autoimmune disease.  
 XX  
 PS Claim 10; Page 71-72; 85pp; French.  
 XX  
 CC The present sequence represents a human protein expressed in tumour  
 CC cells. The polynucleotide is useful for screening cDNA/genomic DNA banks  
 CC and for cloning isolated DNA, identifying mutant forms of the gene that  
 CC encodes a human protein, where the mutations are associated with  
 CC abnormal gene expression, or promoters and regulators of the gene,  
 CC particularly for diagnosis; for recombinant expression of the derived  
 CC protein; as probes and primers for detection and amplification; and  
 CC as antisense therapeutics. The tumour expressed protein is useful for  
 CC raising specific antibodies and to screen agents that modulate its  
 CC activity, bind to it or interact with it. These agents are potentially  
 CC useful for treatment or prevention of diseases associated with abnormal  
 CC expression/activity of the protein, particularly immunological diseases  
 CC (autoimmune diseases and cancer) or viral, bacterial, fungal or parasitic  
 CC infections.  
 CC  
 XX  
 SO Sequence 209 AA;  
 Query Match 21.2%; Score 1169; DB 22; Length 209;  
 Best Local Similarity 99.5%; Pred. No. 8.8e-84;  
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 310 QCDPDKYSEKSSGSSCNVRACIDKDYFTHTACDANGETOLMYAKPKICSEDLBGA 369  
 DB 1 QCDPDKYSEKSSGSSCNVRACIDKDYFTHTACDANGETOLMYAKPKICSEDLBGA 369  
 QY 370 LPAAGVKTHCPNCGFETKTNSTQCPQPYGSYNSGSDCTRCBPAGTEPAVGEFKMMNTL 429  
 DB 61 LPAAGVKTHCPNCGFETKTNSTQCPQPYGSYNSGSDCTRCBPAGTEPAVGEFKMMNTL 429  
 QY 430 PTNMTTVLSGINFERYKMGTEVAGDHIYTAAGASDNDMILLVLPGRPPQSVMAOT 489  
 DB 121 PTNMTTVLSGINFERYKMGTEVAGDHIYTAAGASDNDMILLVLPGRPPQSVMAOT 489  
 QY 490 ENKEVARITFEFTLCSVNCLEYMVGVN 518  
 DB 181 ENKEVARITFEFTLCSVNCLEYMVGVN 518

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